STIC-Biotech/ChemLib

From:

Chan, Christina

Sent:

Wednesday, October 01, 2003 4:35 PM

To:

Subject:

Schnizer, Holly; STIC-Biotech/ChemLib RE: Request for RUSH sequence search for Appl. no. 09/444,281

Importance:

High

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

Fr m:

Schnizer, Holly

Sent:

Wednesday, October 01, 2003 4:26 PM

To:

Chan, Christina

Subject:

Request for RUSH sequence search for Appl. no. 09/444,281

I would like to request the following RUSH sequence search for the above appl. which is an amended due this biweek (Oct. 6).

Please search the commercial and interference databases for the peptide of SEQ ID NO:85 (ILPWKWPWWPWRR)

Thank you.

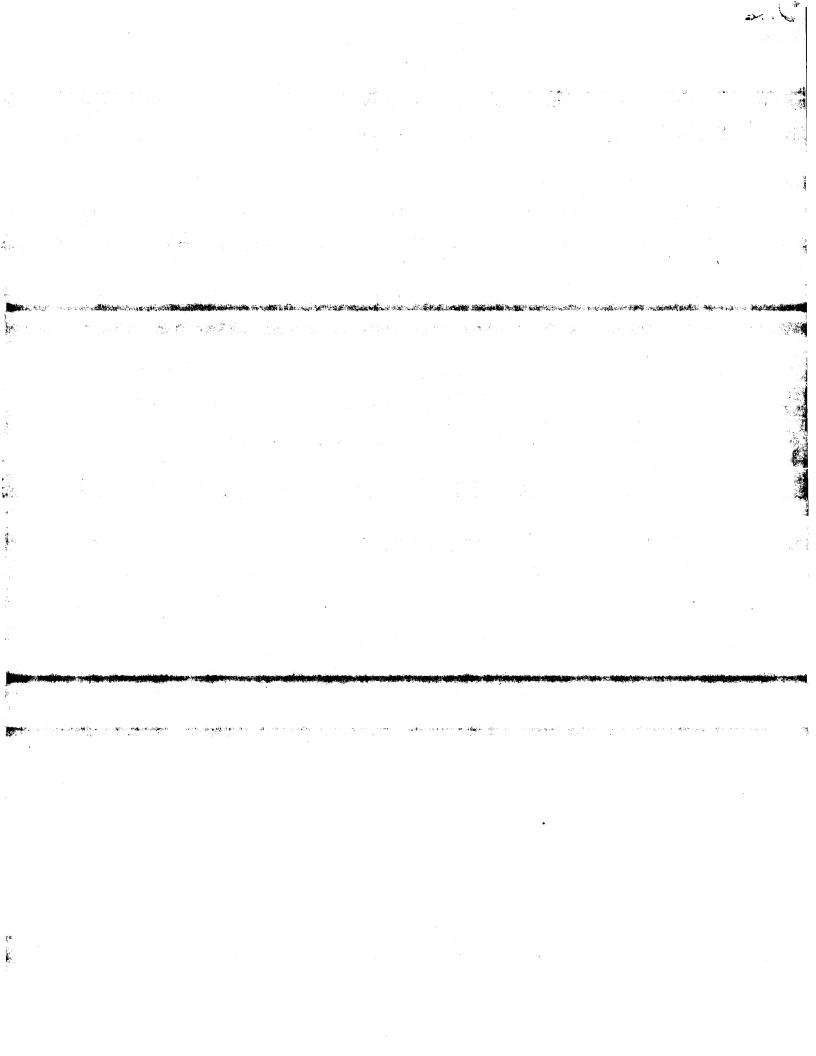
Holly Schnizer AU 1653 CM1-9E09 305-3722

mailbox: CM1-9B01

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

/ENDOR/COST (w	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	



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Title:
Perfect score:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 ~ 2003 Compugen Ltd.
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AAR78457
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ALIGNMENTS

AAR30970 standard; peptide; 13 Ā

AAR30970;

25-MAR-2003 12-MAY-1993 (updated)
(first entry)

Broad spectrum antimicrobial indolicidin peptide

Tryptophan rich; microbial; microbistatic; inhibition.

Bos taurus.

23-DEC-1992

WO9222308-A1

10-JUN-1992; 92WO-US04920

14-JUN-1991; 91US-0715271

(REGC) UNIV CALIFORNIA

Cullor JS, Selsted ME

WPI; 1993-017896/02.

RESULT 1
AAR30970
ID AAR30970
ID AAR3
XX AAR3
AC AAR3
DT 25-M
DT 12-M
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XX REC
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XX Broa
PT comp Broad spectrum antimicrobial cpd. obtd. from bovine granulocytes -comprises tryptophan rich peptide, pref. having low immunogenicity and comprising proline rich peptide or carboxy terminal amide

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ARRESULT 2
ARAPRA 27
AND ARAPRA 27
ARAPRA 
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Matches 13
These analogues exhibit broad spectrum antimicrobial activity and have antimicrobial selectivity when compared to naturally occuring indolicidin. The antimicrobial activity of these analogues can be altered by incorporation of D-form, chemically altered or synthetic amino acids. These sequences can be incorporated into a pharmaceutical composition (e.g. as a liposome or non-liposome lipid complex carrier) for use in a microbicidal method. These sequences are active against gram positive and negative bacteria, protozoa, yeast, fungi and viruses. They can be used as therapeutic agents, prophylactics, food preservatives, disinfectants or medications. These sequences are easily synthesised in an active and effective broad spectrum antimicrobial form
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CC (I)-(VIII) containing up to 25 amino acids (aa): RXZXXZXB (II), BRZXXZXB (III), BRZXXZXB (III), BYZXXZXBB (II), BYZXXZXBB (II), BYZXXZXBBB (AA), MMILBBAGS (IV), BYZXXZXBB (AA), MMCC (IV), LBAXZXXZXBXXBX (VII), KXXZXXZXRRK (VII) and BAZXXXZXBBB (AA), MMCC (V), LBAXZXXXXBXRK (VII) and BAZXXXZXBBB (AX), MMCC (V), LBAXZXXXXBX (VII), AT Least 1 Z = V; CC preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V; CC infections caused by bacteria (Gram positive or negative, or anaerobic); fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or CC trematodes) or viruses. Typical of very many pathogens that can be CC controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola CC hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus CC aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds CC derived from the analogues may be used similarly; the compounds may CC desived the analogues may be used similarly; the compounds may compounds may be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with decreased undesirable side effects. Compared to naturally occuring indolicidin, these analogues show increased antimicrobial and decreased haemolytic activity. Peptide stability, and period of activity within the cell can be increased or decreased according to the incorporation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indolicidin; bacterial infection; photo-oxidised solubiliser; antimicrobial; antibiotic; antiarrythmic; surface disinfectant; additive; shampoo; soap; insecticide; herbicide; preservative; food; technical material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D- or L-form amino acids.
                                                                                                                                                                                                                                                                                                                                                 nucleic acid - vectors, transformed cells and antibodies, conjugates with polyoxyalkylene glycol and fatty acid to toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-1997;
21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY24608 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                      Example 1; Page 32; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          New indolicidin analogues with antimicrobial activity and related
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-169090/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROLOGIX BIOTECH INC
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser JR,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
9.8e-07;
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10-MAR-1997;
20-AUG-1997;
26-SEP-1997;
                                                                                                                                                                                                         AAW66393 to AAW66469 represent native cationic peptides from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has against a microorganism that is tolerant, inherently resistant, or has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administreed by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds
                                                                                                                                                                    acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fundi, narasitor and rise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                Sequence
                                                                                                                                                                 e.g. bacteria, fungi, parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 10; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-520800/44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteria; fungus; parasite; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indolicidin analogue; resistance; cationic peptide; antibiotic;
bacterial infection; tolerance; antibacterial; microorganism;
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  1 Similarity
13; Conser
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100.0%; ilarity 100.0%; Conservative 0
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97US-0040649.
97US-0915314.
97US-0060099.
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. 9.8e-07;
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9.8e-07;
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                                                   Length 13;
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RESULT 5
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                                                                                                                                                         The invention relates to mass production of antimicrobial peptides. The commethod comprises constructing a fusion gene containing a first gene encoding a negatively charged acidic peptide having at least two cysteine cresidues, and a second gene encoding a positively charged basic antimicrobial peptide. A host microorganism is transformed with a vector containing the fusion gene and then cultured. The expressed antimicrobial peptide is then recovered. The method is used to mass produce antimicrobial peptide is then recovered antimicrobial peptide upon the growth of the host confect of the expressed antimicrobial peptide upon the growth of the host confect of the expressed antimicrobial peptide upon the growth of the host confect of the issue of the fusion gene provides an economic, recombinant alternative of mass producing antimicrobial peptides, which overcomes the considerably recombinant and chemical methods. The present sequence represents an antimicrobial peptide Indolicidin. The encoding DNA consistency is the finite of the acidic peptide Guamerin gene in the
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New method for mass production of antimicrobial peptides - by constructing fusion genes comprising acidic and antimicrobial peptide genes and transforming host with vector containing these
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28-MAY-1997;
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                                                                                          Sequence
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N-PSDB; AAV83788.
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                                                                                                                                            construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 18; 52pp; English.
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Conservative
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97KR-0021312
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                                                                                                                                               fusion
                    100.0%;
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                      Score 99; DB 20;
Pred. No. 9.8e-07;
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RESULT 6
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stability against plant protease degradation. Expression of antimicrobial peptides in transgenic plants suffers a major limitation in that the foreign peptides are susceptible to rapid degradation by proteases. The invention concerns reducing the extent of protease degradation of a protein applied to, or produced by a plant by administering indolicidin, Rev4 or a functional equivalent to the plant. Transgenic plants expressing indolicidin and Rev4 are useful for production of the antimicrobial peptides. Compositions containing indolicidin and Rev4 are
                          AAY91740;
                                                                  AAY91740 standard; Peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indolicidin is a potent antimicrobial tridecapeptide, originally purified from cytoplasmic granules of bovine neutrophils. A reverse peptide, Rev4 (AAY92796) of indolicidin was found to have increased
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Pred. No. 9.8e-07;
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                                                                                    Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.
                                                               Synthetic
                                                                                                                                                       Amino acid sequence of cationic peptide MBI 10.
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breast; lung;
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                                                                  Novel pharmaceutical composition polyoxyalkylene-modified cationic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                     tumours
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Disclosure; Page 14; 94pp; English

The patent discloses crosslinked analogs of indolicidin (Indol 1-13) which is a naturally occurring peptide isolated from bovine neutroph and has antimicrobial activity. The crosslinked indolicidin (x-indolicidin) analogs are stable and have antimicrobial activity

negative bacteria

(e.g.

Staphylococcus aureus

neutrophils

against gram positive and

Crosslinked indolicidin analogs with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses

Claim 3; Page 39;

53pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.
                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1; gram positive bacteria; gram negative; Staphylococcus aureus; Escherichia coli; Salmonella typhimurium; yeast; fungi; protozoa; Candida albicans; Cryptococcus neoformans; Giardia; Acanthamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                               stability; bovine neutrophil; antimicrobial; antibacterial; fung
protozoacide; virucide; anti-HIV; human immunodeficiency virus-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crosslink-stabilised indolicidin analog Indol 1-13(W6/9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                   Selsted
                                                                                                                                                                                                                         20-MAY-1999;
                                                                                                                                                                                                                                                23-DEC-1999
                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crosslinked indolicidin analog; X-indolicidin; Indol 1-13(W6/9);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY44666 standard;
                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                   18-JUN-1998;
                                                                                                                                                                                                                                                                      WO9965510-A1
                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                           sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a cationic peptide amino acid sequence,
                                                                                                                             2000-147133/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ILPWKWPWWPWRR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ILPWKWPWWPWRR 13
                                                                                                                                                    ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                  Osapay K;
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                                                                                                                                                                                                                         99WO-US11165
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 6..9
                                                                                                                                                                                                                                                                                                               di-tryptophan crosslink"
                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                             /note= "Residues at positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                            "C-terminal
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                                                                                                                                                                                                                                                                                            amide"
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                                                                                                                                                                                                                                                                                                                               form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungicide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Matches
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli and Salmonella typhimurium), yeasts and fungi (e.g. Candida albicans, Cryptococcus neoformans), protozoa (e.g. Giardia species and Acanthamoeba species), and viruses (e.g. HIV-1).
They can be used for reducing or inhibiting the growth or survival ommicroorganisms in an environment e.g. a food or food product, a solution, an inanimate object comprising a surface, or a mammal. The present sequence is a specifically claimed x-indolicidin analog, Indol 1-13(W6/9) which contains a di-tryptophan crosslink.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purF gene; glutamine pyrophosphoribosyl pyrophosphate amidotransferase; purF derivative; fusion partner; antimicrobial peptide; Indolicidin; mass production; cleavage site; hydroxylamine; CNBr; DNA construct; cow neutralise; toxicity; pharmaceutical industry; food industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY44324 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial
                                                                 The present amino acid sequence is an antimicrobial peptide, Indolicidin derived from cow, Bos taurus. It is used along with a derivative of purF gene sequence that functions as a fusion partner. A DNA construct that comprises, this antimicrobial peptide encoding sequence and the entire, partial or derivative of purF gene, is used for mass production of the antimicrobial peptide in microorganisms without killing the host cells. Use of the purF gene derivative sequence, neutralises the toxicity of the antimicrobial peptides against the host microorganism. The antimicrobial peptides are useful commercially in the pharmaceutical and food industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1998;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                   Kim JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999
                                                                                                                                                                                                                                  Claim 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                               (SAMY-)
                                          Sequence
                                                                                                                                                                                                                                                             in microorganism hosts
                                                                                                                                                                                                                                                                           New DNA constructs useful for mass production
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                                                                                                                                                                                                                                                                                                                                                   Kang MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 AA;
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                                           13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide,
                                                                                                                                                                                                                                                                                                                                                                                                             98KR-0022117.
99KR-0017920.
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                                                                                                                                                                                                                                                                                                                                                      Lee J,
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 100.0%;
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Pred. No.
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    . 99;
No.
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9.8e-07;
    DB 21;
9.8e-07;
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                                                                                                                                                                                                                                                                                 of antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                           Hong
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                  Length 13;
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                                                                                                                                                                                                                                                                                                                                                            Lee
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RESULT 12
AAY55056
ID AAY55
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                                                                                                                    CC The invention relates to a method for inhibiting growth of CC sulphate-reducing bacteria (A) on a matterial (B) sensitive to corrosion CC sulphate-reducing bacteria (A) on a matterial (B) sensitive to corrosion CC degradation, by applying to (B) a bacterium (C) that secretes a CC compound (I) able to inhibit growth of (A). The method is used to protect compound (I) able to inhibit growth of (A). The method is used to protect compound (I) able to inhibit growth of (A). The method is used to protect compound (I) able to inhibit in growth of (A). The method is used to protect compound (I) able to inhibit ing (A) and reduces the amount of toxic chemicals compound (I) and addition of (C) to the biofilm prevents this. A CC growth of (A), and addition of (C) to the biofilm prevents this. A CC growth of (A), and addition of (C) to the biofilm prevents this. A CC growth of (A), and addition of (C) to the biofilm prevents this. A CC growth of (A), and addition of (C) to the biofilm prevents this. A CC growth of (A), and addition of (C) to the biofilm prevents this. A CC growth of (A), and addition of (C) to the biofilm prevents this. A CC growth of (A) are required and inhibit (A) without significant exactly where they are required and inhibit (A) without significant to conventional biocides, which may then be used in reduced compounts). If local damage to the biofilm occurs, the underlying areas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                               Query Match
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Matches 13
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31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indolicidin; bactenecin; sulphate-reducing bacteria; growth inhibitor;
corrosion; degradation; metal; concrete; cement; dental implant; biofilm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-amidated indolicidin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting growth of sulphate-reducing bacteria using particularly for protection of metals and concrete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 41; 84pp; English.
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TK,
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                                  Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILPWKWPWWPWRR
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    ILPWKWPWWPWRR 13
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                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0074037
99US-0282277
                                                                                                AA;
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                                                 100.0%;
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                                       0;
                                                     Score 99;
Pred. No. 9
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                                       Mismatches
                                                        9.8e-07;
                                                                          DB 21;
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                                                                       Length 13;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other bacteria,
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                                            Gaps
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RESULT 13
AAY57123
                                                            provided that if Xaal is present, Xaa8 = Hse, Met or Met-Xaa9-Met;
CC and further provided that: if Xaa2 is absent, Xaal is absent; if Xaa3 is
CC absent, Xaal and Xaa2 are absent; if Xaa4 is absent, Xaa1, Xaa2 and Xaa3
CC are absent, and if Xaa5 is absent, Xaa1, Xaa2, Xaa3 and Xaa4 are absent.
CC The indolicidin analogues can be used to create a fusion polypeptide
CC consisting of the analogue linked to a peptide. The indolicidin
CC analogues have antimicrobial activity against gram positive bacteria,
CC gram negative bacteria, yeast, fungus, protozoa and viruses (e.g. HIV-1).
CC They are also active against helminths. The analogues can be used for
CC creducing or inhibiting growth or survival of a microorganism. They can be
CC used for treating infections. They can also be included in a liquid such
CC as water or an aqueous solution, e.g. contact lens solution. The
CC analogues have potential uses in food products, and in objects such as
CC the surface of an instrument used to prepare food or to perform surgery.
CC Transgenic plants or animals useful in the food industry can be produced
CD into the Germinal in Call of the Company of the company in Call of the Company in Company in Company in Call of the Company in Company 
                                                                                                                                                                                                                                                                                                                                                                                                                                               Xaa4 = Trp, Phe or absent;
Xaa5 = Arg, Lys or absent;
Xaa6 = Trp or Phe;
Xaa7 = Arg, Lys or absent;
Xaa8 = homoserine (Hse), Met, Met
Xaa9 = at least one amino acid;
provided that if Xaa1 is present,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is a naturally occurring indolicidin peptide. Peptides AAY57109-Y57138 and AAY57143-Y51448 are new indolicidin repides AAY57109-Y57138 and hayse and/or a truncated amino remalogues, which have a homoserine residue and/or a truncated amino terminal region. The analogues have the following amino acid sequence: Xaa1-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6-Pro-Xaa6-Pro-Xaa6-Pro-Xaa6-Xaa7-Xaa8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xaal = Ile, Leu, Val, Ala, Gly
Xaa2 = Ile, Leu, Val, Ala, Gly
Xaa3 = Pro or absent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indolicidin analogue; antimicrobial activity; helminth; bacteria; virus; treatment; inhibit growth; micro-organism; contact lens solution; transgenic plant; surgical instrument; yeast; fungi; protozoa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 28; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protozoa and virus, used for, e.g. treating infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1998;
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                                               germline
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                                               cells of such organisms
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Sequence

13

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RESULT 14
ABP60382
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    Matches
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The invention relates to an ophthalmic composition (I) for storing, cleaning, or disinfecting a contact lens, comprising an indolicidin antimicrobial peptide and a buffer having a halide ion concentration less than 0.85 weight%, based on the total weight of (I) or Good's buffer. (I) is a multipurpose solution for care of a contact lens and is suitable for contact lens disinfection, storage, cleaning, conditioning, rehydrating, moistening and lubricating. (I) is useful for disinfecting the contact lens or contact lens storage vessel such as contact lens vial, contact lens case or a contact lens shipping package by contacting the lens or vessel with a disinfecting solution comprising (I). (I) is useful for packaging a contact lens involving sealing the lens in a container with (I), where the contact lens is not autoclaved. (I) reduces the number of Pseudomonas aeruginosa, Staphylococcus aureus and Serratia marcescens organisms by 3.0 logs or more within 4 hours and the number of Candida
                                                                                                                                                                                                                                    Ophthalmic composition for storing, cleaning, or disinfecting contailens, comprises indolicidin, and buffer having specified halide ion concentration or Good's buffer \,
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                                                                                                                                                                                                          Claim 15; Page 68; 91pp; English.
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CHAPOY L L.
QUINN M H.
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HOKAMA L A.
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Pred. No.
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9.8e-07;
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RESULT 15
ABP60383
  Best Loc
Matches
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                                                                                                                                                                                                                                                        (LARG-) LARGE SCALE BIOLOGY
(STRI ) SRI INT.
(REGC ) UNIV CALLFORNIA.
(WESL-) WESLEY-JESSEN CORP.
(TUSE/) TUSE D.
(MORT/) MORTELMANS K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indolicidin; ophthalmic; disinfection; contact lens; antimicrobial; Pseudomonas aeruginosa; Staphylococcus aureus; Serratia marcescens; Candida albicans; Fusarium solani.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP60383 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                  25-MAY-1999;
The invention relates to an ophthalmic composition (I) for storing, cleaning, or disinfecting a contact lens, comprising an indolicidin antimicrobial peptide and a buffer having a halide ion concentration less than 0.85 weight%, based on the total weight of (I) or Good's buffer. (I) than 0.85 weight% based on the total weight of (I) are good's buffer.
                                                                                                   ophthalmic composition for storing, cleaning, clens, comprises indolicidin, and buffer having concentration or Good's buffer
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                                                                              Disclosure;
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HOKAMA L A.
SELSTED M E.
CHAPOY L L.
QUINN M H.
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                                                                              Page 16; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                   9908-0318195
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Pred. No. 9.8e-07;
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g specified halide ion
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Job time : 78

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contact lens disinfection, storage, cleaning, conditioning, rehydrating, compositioning and lubricating. (I) is useful for disinfecting the contact lens or contact lens storage vessel such as contact lens vial, contact clens case or a contact lens shipping package by contacting the lens or cotselwith a disinfecting solution comprising (I). (I) is useful for cotselwing the lens in volving sealing the lens in a container with cotselwing account of lens involving sealing the lens in a container with cotselwing sealing the lens in a container with sealing the number of candidate cotselwing sealing the same sealing the number of candidates and fusion of sealing sealing the number of candidates and fusion of sealing sealing sealing the number of candidates and fusion of sealing sealing sealing sealing the number of candidates cotself-preserving and requires no additional preservatives or components. (I) sealing sealing
Search completed: October
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:59:37; Search time 41 Seconds (without alignments) 30.493 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-444-281-85 99 1 ILPWKWPWWPWRR 13

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	ō	5 1	4	w	2	1	No.	Result
47	47	47	47	47	47	47	47	47	48	48	48	48.5	49	49	49	49.5	50	50	50	50.5	51	51	51	53	53	53.5	54	99	Score	
47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	48.5		48.5			49.5		0	50.5	50.5	50.5	51.0	51.5	51.5	51.5	53.5	53.5	4.	54.5	100.0	Match	Query
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ATP synthase Fi

ALIGNMENTS

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RESULT 2 VGIHHC VGIHHC E2 91ycoprotein precursor - human coronavirus (strain 229E) R2 91ycoprotein precursor - human coronavirus (strain 229E) N;Alternate names: peplomer 91ycoprotein; S 91ycoprotein; spike 91ycoprotein C;Species: human coronavirus A;Note: host Homo sapiens (man) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000 C;Accession: A34766; S05460 C;Accession: A34766; S05460 R;Raabe, T.; Schelle-Prinz, B.; Siddell, S.G. J. Gen. Virol. 71, 1065-1073, 1990	Query Match 100.0%; Score 99; DB 1; Length 144; Best Local Similarity 100.0%; Pred. No. 7.4e-06; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 ILPWKWPWWPWRR 13	RESULT 1 JC1222 JC1223 JC1223 JC1223 JC1223 JC1223 JC1223 JC1223 JC1223 JC1224 JC1224 JC1224 JC1225 JC1225 JC1226 JC1226 JC1226 JC1226 JC1226 JC1227 JC127 JC1227 JC127 JC127

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A;Title: Nucleotide sequence of the gene encoding the spike glycoprotein of human coronal A;Reference number: A34766
A;Reference number: A34766
A;Reference number: A34766
A;Recession: A34766
A;Recession: A34766
A;Recession: A34766
A;Residues: 1-1173 <RAA>
A;Residues: 1-1173 <RAA>
A;Cross-references: EMBE:X16816; NID:g58926; PIDN:CAA34723.1; PID:g58927
A;Scross-references: EMBE:X16816; NID:g58926; PIDN:CAA34723.1; PID:g58927
A;Experimental source: strain 229E
R;Raabe, T.; Siddell, S.
Nucleic Acids Res. 17, 6387, 1989
A;Title: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique A;Reference number: A34038; MUID:89366667; PMID:2701946
A;Reference number: A34038; MUID:89366667; PMID:2701946
A;Reference number: A34038; MUID:89366667; PMID:2701946
A;Residues: translation not shown
A;Molecula type: mRNA
A;Residues: 1159-1173 <RA2>
A;Cross-references: EMBE:X15654; NID:g58921; PIDN:CAA33680.1; PID:g1334827
C;Superfamily: coronavirus Ez glycoprotein
C;Keywords: glycoprotein; transmembrane protein
F;115-1139/Domain: signal sequence #status predicted <MAT>
F;116-1138/Domain: transmembrane #status predicted <MTN>
F;23,62,98,147,171,176,220,243,326,333,440,484,518,538,542,568,581,587,663,671,930,1015,
hypothetical protein DKFZp434Cl92.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change C;Accession: T12505
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wieman; submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17527
A;Accession: T12505
A;Status: preliminary
                                                                                                                                                                                                                               RESULT
E72851
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-299 < ANS>
A; Cross-references: EMBL: AL096753
A; Experimental source: adult testis; clone DKFZp434C192
C; GenetLcs:
A; Note: DKFZp434C192.1
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A; Cross-references: GB:I
C; Genetics:
A; Gene: AcOrf-13
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_cuange *** vic. C;Accession: T41758
R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z22020; MUID:99281911; PMID:10355780
A;Accession: T41758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACMNPV orf13 - Bombyx mori nuclear polyhedrosis virus (isolate T3) C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV A;Variety: isolate T3
A;Variety: isolate T3
C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-55 -KUR>
A;Cross-references: GB:NC_002772; NID:g14141818; PIDN:NP_115277.1; GSPDB:GN00163
                                                                                                                                                                                                                                                                                                                    Proc. R. Soc. Lond. B Biol. Sci. 268
A; Title: Complete mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                   ATP synthase F0 chain 8 [imported] - Eudromia elegans mitochondrion C;Species: mitochondrion Eudromia elegans C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 17-May-2002 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 17-May-2002 C;Accession: E90626
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A; Residues: 1-331 < KAM>
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                                                                                C; Keywords: mitochondrion
                                                                                                 C; Superfamily: H+-transporting
                                                                                                                  A; Genome: mitochondrion A; Genetic code: SGC1
                                                                                                                                                                                                                                                                              A; Reference number: A99613; A; Accession: E90626
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Similarity 6; Conserv
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                51.5%;
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Score 51; DB 2
Pred. No. 2.5;
0; Mismatches
  0;
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Pred. No.
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N;Contains: protein kinase (EC 2.7.1.37)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Acte: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 24-Sep-1999
C;Accession: 138935; 155438; 137209
R;Kawabata, M.; Chytil, A.; Moses, H.L.
J. Biol. Chem. 270, 5625-5630, 1995
A;Title: Cloning of a novel type II serine/threonine kinase receptor through interaction A;Reference number: A55947; MUID:95197572; PMID:7890683
  A;Map position: 20pter-20qter
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;
C;Keywords: ATP; glycoprotein; phosphotransferase; receptor; transm
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1038/Product: bone morphogenetic protein receptor II #status p
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A; Residues: 1-1038 < KAW>
A; Residues: 1-1038 < KAW>
A; Residues: 1-1038 < KAW>
A; Cross references: EMBL:U20165; NID:g704361; PIDN:AAC50105.1; PID:g704362
A; Cross references: EMBL:U20165; NID:g704361; PIDN:AAC50105.1; PID:g704362
B; Nohno, T.; Ishikawa, T.; Saito, T.; Hosokawa, K.; Noji, S.; Wolsing, D.H
J. Biol. Chem. 270, 22528-22526, 1995
A; Title: Identification off a human type II receptor for bone morphogenetic
A; Reference number: I55438; MUID:95403457; PMID:7673243
A; Accession: I55438
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A; Residues: 1-689 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB72923.1;
A; Experimental source: strain PCC 7120
C; Genetics:
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC1927
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A; Note: Nostoc sp. strain PCC 7120 is a synonym of PC; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #C; Accession: AC1927
C; Accession: AC1927
C; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-827, 'R', 829-1038 <ROS>
A; Cross-references: EMBL: 248923; NID
                                                                                                                                                                                                                                                                                                                                              A:Cross-references: GB:D50516; NID:g807712; PIDN:BAA09094.1; PID:g807713
R:ROSSENZWEİG, B.L.; Imamura, T.; Okadome, T.; Cox, G.N.; Yamashita, H.; ten Dijke, P.; i Proc. Natl. Acad. Sci. U.S.A., 7632-7636, 1995
A;Title: Cloning and characterization of a human type II receptor for bone morphogenetic A;Reference number: I37209; MUID:95372334; PMID:7644468
A;Accession: I37209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone morphogenetic protein receptor II precursor - human N;Alternate names: activin receptor-like kinase type II; N;Contains: protein kinase (EC 2.7.1.37)
                                                                                                                                         A;Gene: GDB:BMPR2; BRK-3; T-ALK; BMPR3; BMPR-II
A;Cross-references: GDB:642243; OMIM:600799
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A; Residues: 1-1038 < NOH>
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                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown
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55.6%;
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Pred. No.
protein receptor II #status
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receptor; transmembrane protein
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Yasuda,
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RESULT 9
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ORF MSV076
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A;Gene:
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A;Title: The genome of Melanoplus sanguinipes entomopoxvirus A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORF MSV076 probable spheroidin - Melanoplus sanguinipes entomopoxvirus C;Species: Melanoplus sanguinipes entomopoxvirus C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;151-170/Domain: transmembrane #status predicted < F;201-08/Domain: protein kinase homology <KIN> F;209-217/Region: protein kinase ATP-binding motif F;55,110,126/Binding site: carbohydrate (Asn) (cova
                                                                                                                                                                                                                                                                                                                                                               C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
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A; Residues: 1-970 <AFO>
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A; Residues: 1-83 <ARN>
                                                                                                                                                                                                                                     A; Title: Evidence for lateral gene transfer between Archaea A; Reference number: A72200; MUID:99287316; PMID:10360571 A; Accession: B72392
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                                                                                                                                                                                                                                                                                                                  Garrett, M.M.; Stewart, A.M.;
                                                                                                                                                                                                                                                                                                                               R; Nelson, K.E.;
                                                                                                                                                                                                                                                                                                                                                                                               hypothetical
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                                                          Similarity 5; Conserv
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66.7%;
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Pred.
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Pred. No. 44;
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Pred. No. 47;
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                                                              Mismatches
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; Pratt, M.S.;
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ferredoxin-NADP reductase (EC 1.18.1.2), long form precursor - bovine
N;Alternate names: adrenodxin reductase
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-7ul-1994 #sequence_revision 18-Oct-1996 #text_change 03-Jun-2002
C;Accession: JT0751; JT0079; JS0390; S03558; PS0003; A29604; S52100
R;Takata, Y.; Sagara, Y.; Kono, A.; Sekimizu, K.; Horiuchi, T.
Biol. pharm. Bull. 16, 1200-1206, 1993
A;Title: Gene structure of bovine adrenodoxin reductase.
A;Reference number: JT0751; MUID:94177140; PMID:8130767
A;Accession: JT0751
A;Accession: JT0751; MUID:94177140; PMID:8130767
A;Accession: JT0751; MUID:94177140; PMID:8130767
A;Residues: 1-498 <7aK>
A;Rote: the authors translated tocrtex
A;Note: the authors translated the codon GTC for residue 205 as Gly
R;Sagara, Y.; Takata, Y.; Miyata, T.; Hara, T.; Horiuchi, T.
J. Biochem. 102, 133-1336, 1987
A;Title: Cloning and sequence analysis of adrenodoxin reductase cDNA from bovin, Reference number: JT0079
A;Accession: JT0079
A;Accession: JT0079
A;Residues: 1-204,211-498 <SAG>
A;Residues: 1-204,211-498 <SAG>
A;Residues: 1-204,211-498 <SAG>
A;Residues: T-204,211-498 <SAG>
A;Contents: revision, insertion of residues 205-210
A;Accession: JS0390
A;Accession: JS0390
A;Accession: JS0390
A;Accession: JS0390
A;Accession: JS0390
A;Accession: JS0390
A;Molecule type: mRNA
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95922
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable glycosyltransferase protein SMb21068 [imported] - Sinorhizobium meliloti (stra:
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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C; Genetics:
A; Gene: SMb21068
A; Genome: plasmid
                       A; Molecule type: mRNA
A; Residues: 56-498 <SA2>
R; Hanukoglu, I.; Gutfinger, T.
Eur. J. Biochem. 180, 479-484,
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A; Title:
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D.H.; Wong, K.;
  NADP-binding
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N.A.; Fisher, R.F.
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A; Residues: 1-296 <VI
A; Cross-references: E
C; Genetics:
A; Map position: 1
C; Superfamily: hypoth
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Biochim. Biophys. Acta 1246, 39-46, 1995
A; Title: Structural and functional characterization of bovine A; Reference number: S52100; MUID:95110846; PMID:7811729
A; Accession: S52100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: a cyanogen bromide peptide binds to adrenoferredoxin R; Nonaka, Y.; Murakami, H.; Yabusaki, Y.; Kuramitsu, S.; Kagamiy Biochem. Biophys. Res. Commun. 145, 1239-1247, 1987 A; Title: Molecular cloning and sequence analysis of full-length A; Reference number: A29604; MUID:87270696; PMID:3038094
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A;Title: Adrenoferredoxin-binding peptide of NADPH-adrenoferredoxin A;Reference number: PS0003; MUID:88184054; PMID:3355838
A;Accession: PS0003
                                                                                                                                                A; Status: prellmin. A; Molecule type: DNA
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T03562
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                                                                                                                                                                                                                                                                    R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkor Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome A;Reference number: Z14955; MUID:97404404; PMID:9256491
A;Accession: T03562
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A;Residues: 1-76, 'r,78-80, 'VWLALTTPRSRMLL',95-123,'RVYRLT',129-204,211-273,'R',275-3
A;Cross-references: GB:M17029; NID:g162628; PIDN:AAA30362.1; PID:g162629
A;Experimental source: adrenal cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 33-41, 'S', 43-62; 260-283, 'TM'; 496-498 <HAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Aug-2002
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C; Species: Rhodobacter capsulatus
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                                                                                                                       EMBL:AF010496; NID:g3128256; PIDN:AAC16215.1; PID:g3128363
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28;
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A;Introns: 44/1
C;Keywords: neuropeptide
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-60/Product: sex-peptide #status experimental <MAT>
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A:Title: Drosophila suzukii contains a peptide homologous to the Drosophila melanogaster A; Reference number: A56547; MUID:93357785; PMID:8353518
A; Accession: A56547
                                                              A;Gene: At2g24010
A;Map position: 2
C;Superfamily: serine carboxypeptidase
                                                                                                                                                                                                                                                       A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84631
                                                                                                                                                                                                                                                                                                                      R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                               probable serine carboxypeptidase II [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: E84631
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A;Gene: FlyBase:Dsuz/SP
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A;Note: sequence modified after extraction from NCBI backbone
A;Note: authors translated the codon TGC for residue 12 as Trp
A;Note: sequence extracted from NCBI backbone (NCBIN:136396)
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A; Residues: 1-60 <SCH>
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C; Date: 21-Jul-1995 #sequence_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex-peptide precursor - Drosophila suzukii N;Alternate names: male accessory gland peptide
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Pred. No.
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Job time : 42 secs

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Pred. No. 1s the number of results predicted by chance to become greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
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EMBL; X67340; CAA47755.1; -.
PIR; JC1222; JC1222.
PDB; 1G89; 17-JAN-01.
PDB; 1G89; 17-JAN-01.
PDB; 1HR1; 31-DEC-02.
Interpro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Amidation; Signal; Pyrrol
3D-structure.
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Indolicidin E
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TISSUE-Bone marrow;
MEDLINE-92392368; PubMed-1520337;
MEDLINE-92392368; PubMed-1520337;
Gel Sal G., Storicl P., Schneider C., Romeo D., Zanetti M.;
Gel Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;
Gel Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                      modified
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Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                      BIOL. Chem. 267:4292-4295(1992).

FUNCTION: POTENT MICROBICIDAL ACTIVITY, ACTIVE AGAINST STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.

TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.

PTM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.

SIMILARITY: BELONGS TO THE CATHELLCIDIN FAMILY.
                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                non-profit institutions as long as its content is in no way dand this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
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YAD3_RHILO
BRB1_RAT
NHG1_PSEPU
ACES_BUNFA
E786_DROME
CN3B_RAT
VGL2_IBVB
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                                   Pyrrolidone carboxylic acid;
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ATP8_MUSVO

ATP8_AYTAM
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ATP8_COLPA
ATP8_CORCR
ATP8_COTJA
ATP8_LATCH
ATP8_LATCH

ATP8_CHICK

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Scoring table:

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MEDLINE=90264837; PubMed=2345367;

Raabe T., Schelle-Prinz B., Siddell S.G.;

"Nucleotide sequence of the gene encoding human coronavirus HCV 229E.";

J. Gen. Virol. 71:1065-1073(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-21262210; PubMed-11369870;
Thiel V., Herold J., Schelle B., Siddell S.G.;
"Infectious RNA transcribed in vitro from a cDNA
coronavirus genome cloned in vaccinia virus.";
J. Gen. Virol. 82:1273-1281(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P15423; P89342;
Q990M4;
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                                                                                                                                                                                                                 Hays J.P., Myint S.H.;

"PCR sequencing of the spike genes of chronologically distinct human coronav J. Virol. Methods 75:179-193(1998).
                                                                                                                                                                                                                                                                                         SEQUENCE OF 98-1113 FROM N.A., AND STRAIN-ISOLATE ATCC VR-74 ISOLATE MEDILINE-99086140; PubMed-9870593;
                                                                                                                                                                                                                                                                                                                                                                       with human coronavirus HCOV-
Submitted (FEB-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Isolate RW Stock,
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                                                                                                                                                        SEQUENCE OF 1159-1173 FROM N.A. MEDLINE=89366667; PubMed=2701946;
                                                                                                                                                                                                                                                                                                                                                                                            "Viral and cellular changes in a human cell line persistently with human coronavirus HCoV-229E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolate PilB;
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                MEDLINE-22440020;
                                                                              Nucleic
                                                                                                "Nucleotide sequence of the human 5 unique regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonavia
                                         INTERACTION WITH ANPEP
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                                                                                                                                         Siddell
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(Rel. 42, Last annotation update)
tein precursor (Spike glycoprotein)
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    B.D.,
                      PubMed=12551991;
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SIMILARITY).
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l; Q66174; (
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PIR;

A34766; VGIHHC.

InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.

Pfam;

PF01601; Corona_S1; PF01601; Corona_S2;

Glycoprotein;

Envelope

protein;

Transmembrane;

Signal;

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"Identification of a receptor-binding domain of human coronavirus HCOV-229E.";
J. virol. 77:2530-2538(2003).
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MEDLINE=22521439; PubMed=12634402;

MEDLINE=22521439; PubMed=12634402;

Breslin J.J., Mork I., Smith M.K., Vogel L.K., Hemmila E.M.,

Breslin J.J., Mork I., Sjoestrom H., Noren O., Holmes K.V.;

Bonavia A., Talbot P.J., Sjoestrom H., Noren O., Holmes K.V.;

"Human coronavirus 229E: receptor binding domain and neutralization.by

soluble receptor at 37 degrees C.";

J. Virol. 77:4435-4438(2003).
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Gallagher T.M., Buchmeier M.J.;
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SUBUNIT: Homotrimer. Darring "family specifically recognitions and the statement of t
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BMR2_HUMAN STANDARD; PRT; Q13073; Q16569; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequenc 15-SEP-2003 (Rel. 42, Last annotate Bone morphogenetic protein recepto (BMP type II receptor) (BMPR-II).
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D1-NOV-1995
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MEDLINE=94303173; PubMed=8030224;
MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.";
Virology 202:586-605(1994).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 38.7 kDa protein in PKI-LEF1 intergenic region.
Autographa californica nuclear polyhedrosis virus (ACMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                               EMBL; L22858; AAA66643.1;
EMBL; L09723; AAA46706.1;
PIR; E72851; E72851.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Identification and characterization of lef-1,
involved in late and very late gene expression.
J. Virol. 67:3481-3488(1993).
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Pred. No. 9.
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ned. No. 9.9;
Mismatches
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10, Last sequence update)
12, Last annotation update)
protein receptor type II precursor

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TGF-beta
J. Med. G
[6]
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        Machado R.D. Pauciulo M.W., Thomson J.R., Lane K. Wheeler L., Phillips J.A. III, Newman J.H., Willis Manes A., McNeil K., Yacoub M., Mikhail G., Rogers Humbert M., Donnai D., Martensson G., Tranebjaerg
                                                                                                     Nat.
[7]
                                                                                                                                                    MEDLINE=20428187: PubMed=10973254;
Lane K.B., Machado R.D., Pauciulo M.W., Thomson J.R.,
Phillips J.A. III, Loyd J.E., Nichols W.C., Trembath R.C., A
Brannon C.A., Conneally P.M., Foroud T., Fretwell N., Gaddip,
Koller D., Loyd E.J., Morgan N.V., Newman J.H., Prince M.A.,
Vilarino Gueell C., Wheeler L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.
J. Biol.
                                                            MEDLINE=21063176; PubMed=11115378;
                                                                                                             "Heterozygous germline mutations in receptor, cause familial primary pulnat. Genet. 26:81-84(2000).
                                                                                                                                                                                                                      VARIANTS PPH1 TRP-118; MEDLINE=20428187; PubM
                                                                                                                                                                                                                                                                                                                                                                                                          [5]
                                                                                                                                                                                                                                                                                                                                                                                                                    "Familial primary pulmonary hypertension (gene PPH1) is caused mutations in the bone morphogenetic protein receptor-II gene.", J. Hum. Genet. 67:737-744(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20395844; PubMed=10903931;
Deng Z., Morse J.H., Slager S.L.,
Kalachikov S., Cayanis E., Fischer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutations
                                                                                                                                                                                                                                                                                                                                                   Thomson J.R.,
Elliott G.C.,
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20473811; PubMed=11015450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawabata M., Chytil A., Moses H.L.; "Cloning of a novel type II serine/threonine kinase receptor through interaction with the type I transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          morphogenetic protein type I receptors.";
J. Biol. Chem. 270:22522-22526(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Substantia nigra;
MEDLINE-95372334; PubMed-7644468;
Rosenzweig B.L., Imamura T., Okadome 'ten Dijke P., Heldin C., Miyazono K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                   "Sporadic primary pulmonary hypertension mutations of the gene encoding BMPR-II, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=95197572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a
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                                                                        IANTS PPH1 ARG-123; SER-123; CHARACTERIZATION OF VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                           Genet.
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                                                                                                                                                                                                                                                                                                                        Machado R.D., Pauciulo M.W., Morgan N.V., Humbert Ward K., Yacoub M., Mikhail G., Rogers P., Newman igenbottam T., Gibbs J.S.R., Egan J., Crozier A., llcock R., Corris P., Loyd J.E., Trembath R.C.,
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                                                                                                                                                                                                                                                                           e gene
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is E., Fischer S.G.,
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PPH1 GLY-485
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                                   Lane K.B.,
Williams
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hypertension.";
                       Rogers
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st R.J., Hode
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primary pulmonary hypertension.";
Am. J. Hum. Genet. 68:92-102(2001).
-i- FUNCTION: BINDS TO HMP-7, BMP-2
BINDING IS WEAK BUT ENHANCED BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP +
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SIMILARITY: BELONGS TO T
TGFB RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder characterized by plexiform lesions of proliferating endothelial cells in pulmonary arterioles. The lesions lead to elevated pulmonary arterial pression, right ventricular failure, and death. The disease can occur from infancy throughout life an it has a mean age at onset of 36 years. Penetrance is reduced. Although familial PPHI is rare, cases secondary to known
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND LIVER.
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TO THE SER/THR FAMILY OF
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dominant
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DOMAIN CARBOHYD CARBOHYD PROSITE; PROSITE; PROSITE; 60; 60; EMBL; VARIANT CARBOHYL BINDING CHAIN MIM; 600799; MIM; 178600; EMBL; D50516; BAA09 EMBL; U20165; AAC50 PIR; I38935; I38935 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). DOMAIN DOMAIN ACT_SITE NP_BIND DOMAIN DOMAIN TRANSMEM DOMAIN SIGNAL ProDom; PD000001; Pfam; PF01064; Activin_recp; Pfam; PF00069; pkinase; 1. Genew; Transmembrane; Receptor; InterPro; InterPro; InterPro; GO:0005887; C:integral to plasma membrane; TAS. GO:0005515; F:protein binding activity; TAS. GO:0007178; P:transmembrane receptor protein serine/threo. Z48923; HGNC:1078; BMPR2 PS00108; PS50011; PS00107; IPR000472; Activin_rec.
IPR000719; Prot_kinase.
IPR002290; Ser_thr_pkinase.
1064; Activin_recp; 1. Transferase; 27 151 172 203 209 230 333 AAC50105.1; BAA09094 CAA88759.1; Glycoprotein; PROTEIN_KINASE_ST; FALSE_NEG PROTEIN_KINASE_DOM; 1. 150 171 1038 504 217 230 230 333 550 618 908 9110 1110 1038 Prot_kinase; 1 PROTEIN_KINASE_ATP; Serine/threonine-protein kii otein; Signal; Polymorphism; POLY-ASN.

N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
C-Y (in PPH1).
/FTIG-VAR_013671.
C-> Y (in PPH1).
/FTId-VAR_013671.
C-> W (in PPH1). POLY-SER. POLY-THR. ATP (BY SIMILA BY SIMILARITY. PROTEIN KINASE ATP (BY SIMILA CYTOPLASMIC POTENTIAL EXTRACELLULAR (POTENTIAL) POTENTIAL (BY SIMILARITY). (BY SIMILARITY). MORPHOGENETIC PROTEIN (POTENTIAL). . . . kinase; ATP-binding;
sm; Disease mutation. (POTENTIAL) RECEPTOR TYPE collaboration

VARIANT

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ATP8_CORCN
ID ATP8_CC
AC Q9TB16
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT 28-FEB
DE ATP 8
OS COTYTH
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or send a
                                                          This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                  "Phylogenetic relationships of the enigmatic hoatzin (Opisthocomus hoazin) resolved using mitochondrial and nuclear gene sequences."; Mol. Biol. Evol. 16:1300-1307(1999).

-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99416451; PubMed=10486983;
Hughes J.M., Baker A.J.;
                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                            ATP8_CORCN Q9TBI6;
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                                        modified
                                                                                                                                                    (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX
-i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + H
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                Corythaixoides concolor (Grey go-away-bird).
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                                                                                                                                                                                                                                                                                                 Corythaixoides
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                                                                                                             SUBCELLULAR LOCATION: Membrane-bound. SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8
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            non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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/FTId=VAR_013682.
N -> K (in ppm.
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Pred. No. 21;
1; Mismatches
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E -> D
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C -> S (in PPH1)
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G -> R (IN REF. 1).
W; 1389923CE574B913 CRC64;
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P08165; Q95KN8;
01-AUG-1988 (Rel
                                                                                                                           MEDLINE=88082777; pubMed=3691502;
Hanukoglu I., Gutfinger T., Haniu M., Shively J.E.;
"Isolation of a cDNA for adrenodoxin reductase (ferredoxin-NADP+
reductase). Implications for mitochondrial cytochrome P-450 syst
Eur. J. Biochem. 169:449-455(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
NADPH:adrenodoxin oxidoreductase, mitochondrial
(EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferr
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Hydrogen ion transport; CF(0); Mitochondrion; SEQUENCE 55 AA; 6485 MW; 973552DB00E918AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenodoxin oxidoreductase from bovine adrenal cortex."; Biochem. Biophys. Res. Commun. 145:1239-1247(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                              TISSUE=Adrenal gland;
MEDLINE=99299392; PubMed=10369776;
                                                                              X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
                                                                                                                                                                                                                                                     TISSUE=Adrenal cortex;
                                                                                                                                                                                                                                                                         SEQUENCE OF N-TERMINUS, AND
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"cDNA sequence of adrenodoxin reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Adrenal cortex;
MEDLINE=89170752; PubMed=2924777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87270696; PubMed=3038094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and sequence analysis of adrenodoxin reductase
bovine adrenal cortex.";
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Sagara Y., Takata Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gene structure of bovine adrenodoxin reductase."; Biol. Pharm. Bull. 16:1200-1206(1993).
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Takata Y., Sagara Y., Kono A., Sekimizu K., Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
MEDLINE=94177140; Pu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. 102:1333-1336(1987)
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Pred. No.
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Vonrhein

С.,

Hanukoglu

Schulz G.

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EMBL; D83475; BAA11921.1; JEMBL; D83473; BAA11921.1; JEMBL; D83473; BAA11921.1; JEMBL; D83474; BAA11921.1; JEMBL; D63474; BAA11921.1; JEMBL; M17029; AAA30362.1; EMBL; M17029; AAA30150.1; EMBL; M170751; JT0751. JT0751. JT0751; JT07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH ADRENODOXIN.

MEDLINE-21264735; PubMed=11053423;

Mueller J.J., Lapko A., Bourenkov G., Ruckpaul K., Heinemann U.;

Mueller J.J., Lapko A., Bourenkov G., Ruckpaul K., Heinemann U.;

"Adrenodoxin reductase-adrenodoxin complex structure suggests electron transfer path in steroid biosynthesis.";

J. Biol. Chem. 276:2786-2789(2001).

-i-FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE MITOCHONDRIAL P450 SYSTEMS. INCLUDING COLOESTEROL SIDE CHAIN CLEAVAGE IN ALL STEROIDOGENIC TISSUES, STEROID 11-BETA HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24 HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).

MEDLINE=20455764; PubMed=10998235;

MEDLINE=20455764; PubMed=10998235;

Ziggler G.A., Schulz G.E.;

Crystal structures of adrenodoxin reductase in complex with NADP+ and "Crystal structures of adrenodoxin reductase in complex of an enzyme MADPH suggesting a mechanism for the electron transfer of an enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The structure of adrenodoxin reductase of mitochondrial P450 systems: electron transfer for steroid biosynthesis."; J. Mol. Biol. 289:981-990(1999).
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                                                                                                        TRANSIT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                     CONFLICT
                                                                                       VARSPLIC
                                                                                                                                             Mitochondrion;
                                                                                                                                                            Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adrenodoxin + NADPH.

COFACTOR: FAD:
PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
SUBUNIT: Monomer.
SUBCLLULAR LOCATION: Mitochondrial matrix.
ALTERNATIVE PRODUCTS:
Event_Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIVER.

CATALYTIC ACTIVITY: Reduced adrenodoxin + NADP(+) = oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Long;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1SOId=P08165-2; Sequence=VSP_003415;
Note=Represents 10-20% of all adrenodoxin reductase mRNAs and
Seems to be inactive;
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PRO0419; ADXEDTASE.
IN transport; Oxidoreductase; Flavoprotein; NADP; FAD;
In transport; Oxidoreductase; Flavoprotein; Oxidoreductase; Fad;
In transport; Oxidoreductase; Flavoprotein; Oxidoreductase; Fad;
In transport; Oxidoreductase; Fad
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QDAYH -> RVYRLT
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 RVYRLT (IN REF. 3).
                                        -> VWLALTTPRSRMLL (IN REF
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PS -> RL (IN REF. 3).
RAAGIRLAVTR -> ARRSAWQSPE (IN REF. 3).
TRAVPTGDVEDL -> HPGSAHWGCGGP (IN REF. 3).
           Score 50;
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RESULT ELO1_HU ID BILL ELO1 LIU ELO1 LI
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Matches 6; Conserv
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Elongation of very long chain fatty acids protein 1 (CGI-88).
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC
(CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit
MTATP8 OR ATP8.
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RA Strausberg R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Strausberg R.D., McGernan K.J., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;
RGeneration and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

1- FUNCTION: Could be implicated in tissue-specific synthesis of very
C. conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or
C. conversion of beta-ketoacyl CoA to the saturated acyl CoA or
C. cordiction of trans-2-encyl CoA to the saturated acyl CoA
C. rediction of CACTION: Integral membrane protein. Endoplasmic
C. rediction (By similarity).
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Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin
"Identification of novel human genes evolutionarily
Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
                                     SITE
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                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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 CONFLICT
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SIMILARITY: BELONGS TO THE I
CAUTION: Ref.1 sequence difi
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RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RJ Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Blake J., Boido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bojunga N., Carrinci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lee N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20253178; PubMed=10791983; Tvrdik P., Westerberg R., Silve S., Asadi A. Loison G., Jacobsson A.; "Role of a new mammalian gene family in the chain fatty acids and sphingolipids."; J. Cell Biol. 149:707-718(2000).
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28-FEB-2003 (Rel. 41, Last sequence update)
15-FEB-2003 (Rel. 42, Last annotation update)
Elongation of very long chain fatty acids p
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Mammalia; Eutheria;
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Strausberg R.L., Feingold E.A., Grouse L.H.,
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Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Lunalyυια; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus. NCBI_TaxID=8049;
                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase
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P15996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001)
                                                          Gadus morhua (Atlantic Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wynshaw-Boris A., Yoshida K., Hasegawa
                                                                                             MTATP8 OR ATP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reticulum (Potential).

TISSUE SPECIFICITY: Expressed in a broad variety of tissues.

Highly expressed in stomach, lung, kidney, skin and intestine.

Moderately expressed in white adipose tissue, liver, spleen,
brain, brown adipose tissue, heart and muscle. Weakly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            long chain fatty acids and sphingolipids. May catalyze one of the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE ELO FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reduction of trans-2-enoyl CoA to the saturated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Could be implicated in tissue-specific synthesis
                                                                                                                                                                                     _GADMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collabsen the Swiss Institute of Bioinformatics and the EMBL outst
Suropean Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1858959;
                                                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF170907; AAF72572.1; -. BC006735; AAH06735.1; -. AK003743; BAB22975.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF01151;
                                                                                                                                                                                                                                                                                                                   Similarity 6; Conser
                                                                                                                                                                                                                                                             ALPMSM-MM
                                                                                                                                                                                                                                                                                       ILPWKWPWW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002076;
                                                                                                                                                                                                                                                                                                                                                                         78
279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ring B.,
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                     STANDARD;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNS1_SUR4.
                                                                               cod)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
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POTENTIAL.
POTENTIAL.
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L; Mismatches
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ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
YE -> MR (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                DВ
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                                                                                                                                                                                                                                                                                                                                                Length 279;
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MBL outstation -
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Best Local
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P48179;
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TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (AC MTATP8 OR ATP8.

Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and
                                                                                                                                     SPECIES=0.mykiss; TISSUE=Liver; MEDLINE=96139027; PubMed=8587139;
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosi
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
NCBI_TaxID-8022, 8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X17659; CAA35655.1; -. EMBL; X99772; CAA68110.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Membrane-bound.
-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete mitochondrial DNA sequence of Atlantic cod (Gadus morhua): relevance to taxonomic studies among codfishes.";
MOI. Mar. Biol. Biotechnol. 5:203-214(199)
-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NOMENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.

-i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            morhua."
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmo salar (Atlantic salmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00895; ATP-synt_8;
                                                                                "The
                                                                                                                Zardoya R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001421; ATPase8_mit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96414925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
    rainbow trout, Oncorhynchus dol. Evol. 41:942-951(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H(+)(Out)
                            oya R., Garrido-Pertierra A., Bautista J.M.; complete nucleotide sequence of the mitochondrial rainbow trout, Oncorhynchus mykiss.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S08424;
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.5%;
83.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E85C81E63DB48B15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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                                                                        DNA genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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OC Dipnoid
OC Eukary
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OX NCBL_T
RN [1]
RP SEQUEN
RC TISSUE
RX MEDLIN
RA Zardoy
RT TUNGFI
RT Close
RI Close
RI Geneti
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete mitochondrial genome sequence of a teleost, Salmo salar and comparisons with other salmoniformes.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-i- CATALTIC ACTIVITY: ATP + H(2)O + H(+)(In) - ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L29771; AAB03351.1; -.
EMBL; U12143; AAD04737.1; -.
EMBL; AF133701; AAF61382.1;
PIR; T09861; T09861.
PIR; T09951; T09951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.salar; TISSUE*Liver;
MEDLINE=20018174; PubMed=10548724;
Hurst C.D., Bartlett S.E., Davidson W.S., Bruce I.J.;
"The complete mitochondrial DNA sequence of the Atlantic salmon, salar.";
                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
ATP synthase protein 8 (EC 3.6.3.14) (ATPas
MTATP8 OR ATP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001421; ATPase8_mit.
pfam; pF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion;
TRANSMEM 4 24 POTENTIAL.
              "The complete nucleotide sequence of the mitochondrial genome lungfish (Protopterus dolloi) supports its phylogenetic positiclose relative of land vertebrates.";
                                                                                                                                                                                                                                                                                                       ATP8_PRODO Q35416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                              Zardoya R., Meyer
                                                                                MEDLINE=96271539;
                                                                                               TISSUE=Egg
                                                                                                                SEQUENCE
                                                                                                                                            NCBI_TaxID=27779;
                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                             Mitochondrion.
                                                                                                                                                                                                         Protopterus dolloi (Lungfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arnason U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.salar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H(+)(Out)
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                                                                                                                                                                                                                                                                                                                                                                                                        49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                              Lepidosireniformes;
                                                                                                                                                                                                                                                                                                                                                                                                        PWNWPW 54
                                                                                                              FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                      PWKWPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnsson E., Rasmussen A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                PubMed=8846902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6413 MW;
                                                                                                                                                                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                              Protopteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D02920C3E346925F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB Pred. No. 4.7;
                                                                                                                                                                           Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                        n update)
(ATPase
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                                phylogenetic position
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                                                                                                                                                                           Euteleostomi;
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COMPONENT

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RESULT 13
ATP8_SALL
ID ATP8_SAL
ID ATP8_SAL
ID ATP8_SAL
ID 16-CCT
DT 16-CCT
DT 16-CCT
DT 16-CCT
DT 28-FEB
DE ATP SEB
DE ATP SEB
OCC ACLINO
OC EUKATY
GN MITATP8
OC NCBL_T
RN [1]
RP SEQUEN
RA DOITON
RA COMMIL
CC -!- SU
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001421; ATPase8_mit.
pfam; pF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPC
(CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit MTATP8 OR ATP8 OR ATPASE8.
Salvelinus alpinus (Arctic char).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L42813; AAC38025.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0), SUBBUNI) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9XN27;
                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doiron S., Blier P.U., Bernatchez L.;
"A comparative analysis of complete sequence of mitochondrial genome between brook char (Salvelinus fontinalis) and arctic char (S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP8_SALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpinus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion
                           InterPro; IPR001421; ATPase8_mit.
Pfam; PF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mi
                                                                                                                 EMBL; AF154851; AAD41389.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H(+)(Out)
                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Membrane-bound SIMILARITY: BELONGS TO THE ATPASE PRO
                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                              BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ort; CF(0); Mitochondrion; 6523 MW; 95343043B5B2DC53
         6455
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         CF(0); Mitochondrion; MW; 71E430C2E346924A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
            Transmembrane CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 14
ATP8_SALFO
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AT ATP8_SC
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Best Local
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Best Local
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
WMATP8 OR ATP8 OR ATPASE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpinus).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Doiron S., Blier P.U., Bernatchez L.;

"A comparative analysis of complete sequence of mitochondrial between brook char (Salvelinus fontinalis) and arctic char (S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salvelinus fontinalis (Brook trout) (Brook char)
                    ATP8_SCYCA STANDARD; PRT; 55 AA.

679405;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP8 synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L)
MTATP8 OR ATP8 OR ATPASE8.

SCYLIOTHINUS canicula (Spotted dogfish) (Spotted catshark).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protacanthopterygii;
NCBI_TaxID=8038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001421; ATPase8_mit.
Pfam; PF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mi
                                                                                                                                                                                                                                                     SCYCA
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PIR; T11304; T11304.
InterPro; IPR001421; ATPase8_mit.
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Pfam; PF00895; ATP-synt_8; CF(0); Mitochondrion; Transmembrane.
Hydrogen ion tansport; CF(0); Mitochondrion; Gransmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delarbre C., Spruyt N., Delmarre C., Gallut C., Barriel V.,
Janvier P., Laudet V., Gachelin G.;
"The complete nucleotide sequence of the mitochondrial DNA of the
dogfish, Scyliorhinus canicula.";
Genetics 150:331-344(1998).
-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
(CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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Q8pbi7 xanthomonas
Q96be4 homo sapien
Q9dt81 tt virus. o
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ALIGNMENTS

							
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Nature 417:459-463(2002). EMBL; AED12102; AAM39407.1; - Hypothetical protein; Complete proteome. SEQUENCE 780 AA; 85074 MW; 12867434D1852549 CRC64;	Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities":	Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,	.M., K , Mach , Mei	Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Fereira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Gregolo C.C., Gruber A.,	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-ATCC 33913 / NCPPB 528; MEDLINE-22022145; PubMed-12024217; MEDLINE-22022145; PubMed-12024217; da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,	Hypothetical protein XCC0088. XCC0088. Xanthomonas campestris (pv. campestris). Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas. NCBL_TaxID=340;	1 8PE93; 1-OCT-2002 1-OCT-2002 1-OCT-2002

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Pfam; PP02956; TT_ORF1; 1.
PROSITE; PS00131; CARBOXYPEPT_
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 Okamoto H., Nishizawa T., Tawara
Sai T., Sugai Y.;
"TT virus mRNAs detected in the
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Virology 277:368-378(2000).
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zawa T., Tawara A.,
                                                       Res. Commun.
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75.0%;
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                                                                                                                                                                                                                                                unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB Pred. No. 13; 0; Mismatches
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Last annotation update)
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Last annotation updat
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Pred. No.
     1DA6F8F1AB69AA43 CRC64;
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                                                                                                                                                                                                                                                    ssDNA viruses
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 723;
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Best Local S
Matches 8
RP SEQUENCE FROM N.A.

RP STRAIN-ATCC 33913 / NCDPB 528;

RC STRAIN-ATCC 33913 / NCDPB 528;

RX MEDLINE-22022145; PubMed=12024217;

RA DIVER A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Cammargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Cammargo L.E.A.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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01-JUN-2002
01-MAR-2003
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EMBL; AF403185; AAL87800.1; -.
InterPro; IPR00631; Tat
TIGRPAMS; TIGR01409; TAT_signal_seq;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Las
Hypothetical 16.9 kDa protein.
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NCBI_TaxID=49338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein SEQUENCE 152 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8PBI7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-DCB-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=340;
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21,
23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2F5A00F01E70A379 CRC64;
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No.
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3.6;
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9.7;
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RESULT 7
Q90781
ID Q90781
ID Q9070
AC Q9DT
O1 -W
DT 01 -W
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Best Local S
Matches 6
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Best Local
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Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xa host specificities.";
Nature 417.459-463(2002).
EMBL; AE012212; AAM40431.1; -.
InterPro; IPR003709; VanY.
Pfam; PF02557; VanY; 1.
Hypothetical protein; Complete prote SEQUENCE 208 AA; 22940 MW; 10B18
                                                                                                                                                                                                                                                                                                  Q9DT81;
01-MAR-2001
01-MAR-2001
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEDIFENCE (OCT-2001) to the EMBL/GenBank/DDBJ databases Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P.
                                                                                                                                                                                                                                                                                 ORF1
                                                                                                                  MEDLINE=20568739; PubMed=11118348; Okamoto H., Nishizawa T., Tawara A
                                                                                                                                                                                                                 Viruses; ssDNA viruses; NCBI_TaxID=68887;
                                                                                                                                                                                                                                                        TT virus.
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01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96BE4
                                                                                                                                                               STRAIN-TYM9;
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Q9DT81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                  Biochem. Biophys. Res. Commun. EMBL; AB050448; BAB19928.1; -.
                                                          individual
                                                                            "TT virus mRNAs detected in the bone marrow
                                                                                                   Sai T., Sugai Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 55.6%;
Similarity 75.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLPGPWPGWPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWKWPWWP 10
50448; BAB19928.1; IPR004219; TTvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al protein.
342 AA; 37741 MW;
                                                                                                                                                                                                                                                                                                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
  TTvirus_Unk
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22,
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19,
22,
                                                                                                                                                                                                                                          unclassified
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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10B180F6EAF7B014 CRC64;
                                       279:700-707(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3147596F8D7DF849 CRC64;
                                                                                                                    Α.,
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                                                                                                                    Takahashi M.,
                                                                                                                                                                                                                                          ssDNA viruses
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19;
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13;
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                                                                                from
                                                                                                                  Kishimoto
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RESULT 8
Q91D04
ID Q91D
AC Q91D
AC Q91D
DT 01-D
DT 01-D
DT 01-C
DF 01-D
DT 01-C
OK TT v
OK NCBI
RN KCBI
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Q990M4
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Best Local S
Matches 8
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Best Local 9
Query Match
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O990M4;
O1-JUN-2001 (TremBLrel. 1
01-JUN-2001 (TremBLrel. 1
01-OCT-2002 (TremBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91D04;
Q91D04;
01-DEC-2001
01-DEC-2001
01-OCT-2002
                                                                                      "Viral and cellular changes in a human cell li with human coronavirus HCOV-229E."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; AF344186; AAK32188.1; InterPro; IPR002551; Corona_S1. InterPro; IPR002552; Corona_S2.
                                                     Pfam; PF01600; Corona_S1; Pfam; PF01601; Corona_S2;
                                                                                                                                                                                                    STRAIN=229E;
Bonavia A., Holmes K.V.;
                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-str
Coronaviridae; Coronavirus.
NCBI_TaxID=11137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO
Pfam; PF02956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Heterogeneous distribution of multiple tissues from infected willing 288:358-368(2001).
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Yoshikawa A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TT virus.
Viruses; ssDNA viruses;
NCBI_TaxID=68887;
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SEQUENCE 748 AA; 88552 MW;
                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Spike glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   Human coronavirus (strain 229E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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8; Conserv
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                                                                                                                                                                                                                                                                                                                   positive-strand
                                    AA;
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19,
22,
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Pred. No. 38;
1; Mismatches
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                                      ABC6E0A75E8BD8A4 CRC64;
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RESULT OPPORTS OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  덩
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     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q990M3 PRELIMINARY;
Q990M3;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
Spike glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                           "Viral and cellular changes in a human cell line persistently infected with human coronavirus HCOV-229E.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF344187; AAK32189.1; -.
InterPro; IPR002551; Corona_S1.
InterPro; IPR002551; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spike
S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonavia A., Holmes K.V.;

Bonavia A., Holmes K.V.;

with human cellular changes in a human cell line persist

"Viral and cellular changes in a human cell line persist

"Viral and cellular changes in a human cell line persist

"Viral and cellular changes.";

submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF344189; AAK32191.1;

Interpro; IPR002551; Corona_S1.

Interpro; IPR002552; Corona_S2.

Pfam; PF01601; Corona_S1; 1.

Pfam; PF01601; Corona_S2; 1.

SEQUENCE 1173 AA; 128760 MW; B73A165A6270152A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human coronavirus (strain 229E)
Viruses; ssRNA positive-strand
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human coronavirus (strain 229E) Viruses; ssRNA positive-strand Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                                                                                                                             STRAIN=229E;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11137;
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                                                                                                                                                                                                                                                                                                                                   Bonavia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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6; Conser
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                                                                                                                                                                                                                                                                                                                                      Holmes K.V.;
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0; Mismatches
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Mismatches
                                                                                         9E2368160082A81A CRC64;
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RESULT 12
Q990M2
ID Q990M
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DT 01-JU
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DE Spike
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Best Local Similarity
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"Viral and cellular changes
with human coronavirus HCOV-
Submitted (FEB-2001) to the
EMBL; AF344188; AAK32190.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human coronavirus (strain 229E).
Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
                                       STRAIN=Br1/87;
MEDLINE=9338943; PubMed=8397280;
Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.;
"Sequence determination of the nucleocapsid protein gene of the
porcine epidemic diarrhoea virus confirms that this virus is a
                                                                                                                                                                                                                                                                  Porcine epidemic diarrhea virus.
Viruses; ssRNA positive-strand v
Coronaviridae; Coronavirus.
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InterPro; IPR002552; Corona_S2.
Pfam; PF01000; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
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coronavirus related to human coronavirus transmissible gastroenteritis virus."; J. Gen. Virol. 74:1795-1804(1993).
                                                                                                                                        J. Gen. Virol.
                                                                                                                                                                                                                                                                                                                                                                  Q84712;
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                       virus
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01-OCT-2002
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                                                                                                                                                                                Duarte M.,
                                                                                                                                                                                               MEDLINE=94231173;
                                                                                                                                                                                                                                                    NCBI_TaxID=28295;
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                                                                                                                                                                 Duarte M., Laude H.;
Sequence of the spike
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                                                                                                                                                                                                PubMed=8176382;
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17, Last sequence up
22, Last annotation
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[3] SEQUENCE FROM N.A.

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01-DEC-2001
01-DEC-2001
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94120721; PubMed=8291230; Duarte M., Tobler K., Bridgen A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spike protein.
Porcine epidemic diarrhea virus.
                      MEDLINE-98455678; PubMed-9782358; Bridgen A., Kocherhans R., Tobler K., Carvajal A., Ackermann "Further analysis of the genome of porcine epidemic diarrhea Adv. Exp. Med. Biol. 440:781-786(1998).
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Duarte M., Tobler K., Bridgen A.,
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                       "PEDV leader sequence and junction sites."; Adv. Exp. Med. Biol. 380:541-542(1995).
                                                                                                                                                                                                                                         Tobler K., Ackermann M.;
                                                                                                                                                                                                                                                             MEDLINE=96112302; PubMed=8830538;
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                                                                                                                                                                                                                                                                                                                                                            Virology 198:466-476(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93389433; PubMed=8397280;
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Pr01601; Corona_S2; 1.
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85.7%;
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741C84D5DD3BDC4D CRC64;
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genes reveals a polymo
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                                                                                  "Cloning and nucleotide sequence analysis of spike epidemic diarrhea virus detected in Korea."; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ datah EMBL; AY167585; AAN86621.1; SEQUENCE 1383 AA; 151582 MW; B5BA4D7EE5371A54 C
                                                                                                                                                                                                                       Spike protein.
Porcine epidemic diarrhea virus
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                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Chinju99;
                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV777;
                                                                                                                                          Yeo S.-G., Krell P.,
                                                                                                                                                                                     NCBI_TaxID=28295;
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Copyright (c) 1993 - 2003
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Result No.

Database

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ALIGNMENTS

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-715-271-1
                                                                                                                                                                                   TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P3: TELECOMMUNICATION INFORMATION: TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN
STREET: 444 So. Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Selsted, Michael E.
APPLICANT: Cullor, James S.
TITLE OF INVENTION: BROAD SPECTRUM ANTIMICROBIAL COMPOUNDS
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 444 SO. F1
CITY: Los Angeles
STATE: California
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                                                               Similarity 100.
ILPWKWPWWPWRR 13
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US-08-197-205-1

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APPLICATION NUMBER: US/08/197,205

FILING DATE: 16-FEB-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 9-UC 9881

REFERENCE/DOCKET NUMBER: P-UC 9881

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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TITLE OF INVENTION: Broad Spec
TITLE OF INVENTION: and Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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             ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,205
FILING DATE: 16-FEB-1994
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
                                                                                                                                                                                                                                                                                                                APPLICANT: Selsted, Michael E.
TITLE OF INVENTION: Broad Spectrum Antimicrobial Compounds
TITLE OF INVENTION: and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
Local Similarity 100.0%;
hes 13; Conservation
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                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                            CITY: San Diego
                                                                                                                                                                                     COUNTRY:
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CLASSIFICATION:
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                                                                                                                                                                                                         California
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                          EE: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
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16-FEB-1994
1: 514
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Pred. No.
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Best Local Similarity
Matches 13; Conserv
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                Matches
                                                                                                                                                                                                                                    APPLICATION UMBER: US/08/915,314
APPLICATION: 20-AUG-1997
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 36081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
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                                                  Best
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PTELECOMMUNICATION INFORMATION: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CITY: Seattle
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                                                  Local
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                                                                                                                       TOPOLOGY:
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amino acid
GY: linear
1 ILPWKWPWWPWRR 13
                                                Similarity
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                                    Score 99; DB 3;
Pred. No. 1.1e-07;
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US-09-230-180-30
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Best Local (
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APPLICANT:
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PRIOR APPLICATION NUMBER: KR 2
PRIOR APPLICATION DATE: 1997-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Korea Advanced Institute of Science and Technology TITLE OF INVENTION: METHOD FOR MASS PRODUCTION OF TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE FILE REFERENCE: 6181/0F135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-230-180-30
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                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                               APPLICANT: GOUGH, MODISHA
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME
NUMBER OF SEQUENCES: 44
APPLICATION NUMBER: US/08/702, FILING DATE: 23-AUG-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/002,687 FILING DATE: 23-AUG-1995
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           COUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                          ADDRESSEE: fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
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13; Conserv
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Lee, Hyun-Soo
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Kim, Jeong Hyun
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                                                                                                                                                                                                             USA
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Hancock, Robert E. W.
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Pred. No.
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                                                                                                                                                                                                                              RESULT 8
                                                                                         GENERAL INFORMATION:
APPLICANT: Selsted, Micha
APPLICANT: Osephay, Klara
APPLICANT: OSEPHAY
APPLICANTION: Cross
TITLE OF INVENTION: Cross
TITLE REFERENCE: P-UC 305(
SOFTWARE:
SEQ ID NO 1
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/076,227
CURRENT FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 13
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Selsted, michael E.
TITLE OF INVENTION: Indolicidin Analogs and Methods of Using Same
FILE REFERENCE: P-UC 3049
                                                                                                                                                                             Sequence 1, Application US/09099631A Patent No. 6444645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09076227 Patent No. 6303575
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                                               CURRENT APPLICATION NUMBER: US/09/099,631A
CURRENT FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (13)
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TELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER: 38,347
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13; Conservative 0;
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                                                                                              ON: Crosslink-Stabilized Indolicidin Analogs P-UC 3050
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Pred. No.
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Pred. No.
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hes 0;
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; NAME/KEY: MOD_RES; LOCATION: (13); OTHER INFORMATION: AMIDATION US-09-099-631A-1
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US-09-099-631A-3
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CURRENT FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09318195A Patent No. 6482799
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                                                       SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Selsted, Michael E.

APPLICANT: Osapay, Klara
TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs
FILE REFERENCE: P-UC 3050
FILE REFERENCE: P-UC 3050
                                                                                      TITLE OF INVENTION: Self-Preserving Multipurpose Ophthalmic Solutions TITLE OF INVENTION: Incorporating a Polypeptide Antimicrobial FILE REFERENCE: 017942-00.1400US CURRENT EPDLICATION NUMBER: US/09/318,195A CURRENT FILING DATE: 1999-05-25 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                               APPLICANT: Tuse, Daniel
APPLICANT: Mortelmans, Kristien
APPLICANT: Hokama, Leslie A.
APPLICANT: Chapoy, Larry L.
APPLICANT: Quinn, Michael H.
APPLICANT: Large Scale Biology Corporation
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                                                                      SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME, KEY: MOD_RES
LOCATION: (13)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Construct
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ORGANISM: Artificial Sequence
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les 13; Conserv
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1 ILPWKWPWWPWRR 13
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Pred. No.
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Pred. No. 1.1e-07;
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; FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:indolicidin
, OTHER INFORMATION: analog Indol-12-R13-R-OH
US-09-318-195A-2
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US-09-030-619-204
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US-09-030-619-98
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Best Local S
Matches 13
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SEQ ID NO 98
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                                                SEQ ID NO 204
                                                                                                                                                                                                                                                                                                                                               Sequence 204,
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
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APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
APPLICANT: MCNIcol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALG
TITLE OF INVENTION: WITH AMTIBIOTICS
TITLE DEFENCE: GEORGIA AG
                                                               CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 23-
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                   APPLICANT: MCNICOL, PATRICIA J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES AL

TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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ORGANISM: Artificial Sequence
                TYPE: PRT
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ORGANISM: Bos taurus
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13; Conserv
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13; Conserv
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Erfle, Douglas
Fraser, Janet R.
West, Michael H.P.
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Erfle, Douglas
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                                                                                                                                                                                                                                                                                           Krieger, Timothy J.
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nilarity 100.0%;
Conservative 0;
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Pred. No.
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Pred. No. 1.1e-07;
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                                                                                                                                                                        CATIONIC PEPTIDES ALONE OR IN COMBINATION
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hes 0;
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RESULT 14
US-09-667-486-29
; Sequence 29, Application US/09667486
; Patent No. 6538106
; GENERAL INFORMATION:
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US-09-416-481A-1
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Patent No. 6524585
GENERAL INFORMATION:
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Best Local :
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PRIOR APPLICATION NUMBER: US 09/076,227
PRIOR FILING DATE: 1998-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Selsted, Michael E.
TITLE OF INVENTION: Indolicidin Analogs and Methods of Using
FILE REFERENCE: P-UC 3794
CURRENT APPLICATION NUMBER: US/09/416,481A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD_RES
LOCATION: (13)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    APPLICANT: Fraser, Janet R.

West, Michael H.P.
Krileger, Timothy J.

Taylor, Robert
Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED an
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 90
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13; Conserv
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                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                         STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09416481A
                                                                                                      ZIP: 98104
                                                                                                                          COUNTRY:
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Pred. No. 1.1e-07;
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                   Version #1.30
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Search completed: October Job time : 26 secs
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                                                                                                                                                                                             ; OTHER INFORMATION: US-09-076-227-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-667-486-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
TITLE OF INVENTION: Indolicidin Analogs and Methods of Using Same
FILE REFERENCE: P-UC 3049
CURRENT APPLICATION NUMBER: US/09/076,227
CURRENT FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 37 -
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 24
LENGTH: 14
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09076227 Patent No. 6303575
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Best Local
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                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE: NAME/KEY: MOD_RES LOCATION: (14)
OTHER INFORMATION: Xaa is home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                           OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6538106tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                           ch 100.0%; l Similarity 100.0%; 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                            1 ILPWKWPWWPWRR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/667,486 FILING DATE: 22-Sep-2000
                                                              ILPWKWPWWPWRR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                            construct
                                                                                                                                                                                                                                                         Xaa is homoserine (Hse).
                                                                                                                                                                                                                           Description of Artificial Sequence: Synthetic
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Pred. No. 1.1e-07;
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Result
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Maximum Match 10
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Maximum DB
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq
        Published_Applications_AA:*

1: '/cgn2_6/ptodata/2/pubpaa/pt
2: '/cgn2_6/ptodata/2/pubpaa/pt
3: '/cgn2_6/ptodata/2/pubpaa/U
4: '/cgn2_6/ptodata/2/pubpaa/U
5: '/cgn2_6/ptodata/2/pubpaa/U
5: '/cgn2_6/ptodata/2/pubpaa/U
6: ;/cgn2_6/ptodata/2/pubpaa/U
8: '/cgn2_6/ptodata/2/pubpaa/U
9: '/cgn2_6/ptodata/2/pubpaa/U
9: '/cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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(/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
1: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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                                  US-09-030-619-98
US-09-030-619-204
US-09-917-340-13
1 US-09-988-792-5
1 US-09-820-053A-42
1 US-09-820-053A-57
2 US-10-229-368-3
2 US-10-229-368-4
2 US-10-225-087-3
2 US-10-225-087-3
5 US-10-19-171-57
6 US-10-19-171-57
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      US-09-909-652-5
US-09-030-619-40
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(without alignments)
31.643 Million cell updates/sec
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Sequence 98, Appl
Sequence 204, App
Sequence 13, Appli
Sequence 57, Appli
Sequence 57, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 42, Appli
Sequence 57, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
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Sequence 6, Appli
Sequence 6, Appli
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73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73.5	73.5	73.5	75	75	75	75	75.5	75.5	75.5	81	81
73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	74.2	74.2	74.2	Ģ.	75.8	5	75.8	76.3	76.3	76.3	81.8	81.8
13	13	13	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12	13	13	13	28	28	28	28	15	15	15	12	12
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US-10-229-368-6	US-10-229-368-5	US-09-030-619-109	US-09-030-619-99	US-09-030-619-95	US-09-030-619-53	US-10-225-087-77	US-10-225-087-72	US-10-225-087-38	US-10-225-087-20	US-10-229-368-87	US-10-229-368-82	US-10-229-368-41	US-10-229-368-20	US-09-030-619-112	US-09-030-619-73	US-09-030-619-67	US-09-030-619-43	US-10-225-087-37	US-10-229-368-40	US-09-030-619-107	US-10-225-087-32	US-10-229-368-33	US-09-030-619-104	US-09-030-619-50	US-10-225-087-16	US-10-229-368-16	US-09-030-619-39	-10-225-087-	US-10-229-368-17
6,	Sequence 5, Appli	'n	Sequence 99, Appl	•		77,	72	38,		87,	82,	Sequence 41, Appl	e 20,	112,	73,	67,	13,	•	40,	107,	32,	e 33,	•	50,	16,	e 16,	39, 🌶	Sequence 17, Appl	Sequence 17, Appl

ALIGNMENTS

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US-09-030-619-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98, Application US/09030619B Patent No. US20020035061A1 GENERAL INFORMATION:
                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                    SEQ ID NO 98
                                                                        Matches
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSTITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALO
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 560081.406
                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Krieger, Timothy J. APPLICANT: Taylor, Robert
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                 LENGTH: 13
TYPE: PRT
                                                                                                                                                                               FEATURE:
                                                                                                                                                                                            ORGANISM: Artificial Sequence
l Similarity
13; Conserv
                                                                      Conservative
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                                                                          Mismatches
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RESULT 2 US-09-030-619-204

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; TYPE: PRT; ORGANISM: Bos taurus US-09-030-619-204
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                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bos taurus US-09-917-340-13
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                Sequence 5, Application US/09988792 Publication No. US20030032599A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: MCARULTY, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 204
LENGTH: 13
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Best Local Similarity
Matches 13; Conserv
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SEQ ID NO 13
LENGTH: 13
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Best Local :
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APPLICANT: Taylor, Robert
APPLICANT: Erile, Douglas
APPLICANT: Erile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: MCNICOL, Patricia J.
APPLICANT: MCNICOL, Patricia J.
APPLICANT: MCNICOL, PATRICIA J.
APPLICANT: MCNICOL, PATRICIA J.
TITLE OF INVENTION: LIMPECTIONS USING CATTONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/290,932 PRIOR FILING DATE: 2001-05-15
APPLICANT: Lipkowski, Andrezej W
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/917,340 CURRENT FILING DATE: 2001-07-29
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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nes 13; Conserv
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Pred. No.
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Pred. No. 3
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US-09-820-053A-57
; Sequence 57, Application US/09820053A
; Publication No. US20030083243A1
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US-09-820-053A-42
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Best Local S
Matches 13
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SEQ ID NO 5
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
                                                            APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BLOACTIVE PEPTIDES
FILE REFERENCE: HELXO27
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELX027
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TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
FILE REFERENCE: 18475-025
CURRENT APPLICATION NUMBER: US/09/988,792
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,369
PRIOR APPLICATION NUMBER: 60/252,369
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 14
                                  LENGTH: 1:
TYPE: PRT
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OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD_RES
LOCATION: (13)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: AMIDATION
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FEATURE:
               ORGANISM: ARTIFICIAL SEQUENCE
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Pred. No. 3.6e-05;
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Pred. No. 3.6e-05;
Mismatches 0;
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                                                    US-10-229-368-4
                                                                                                                                                                                                                                                                                                                                                                                                               US-10-229-368-4
                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: McNicol, Patricia J.

APPLICANT: Pawlak, Sonia K.

APPLICANT: Rubinchik, Evelina

APPLICANT: Cameron, Dale

APPLICANT: Guarna, Maria Marta

TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY

TITLE OF INVENTION: PEPTIDES

FILE REFERENCE: 660081.418
                                                                                                                               CURRENT APPLICATION NUMBER: US/10/229,368
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/229,368
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
Query Match
Best Local Similarity
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APPLICANT: Guarna, Maria Marta
TITLE OF INVENTION: ANTHMICROBIAL AND
TITLE OF INVENTION: PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McNicol, Patricia J. APPLICANT: Pawlak, Sonia K. APPLICANT: Rubinchik, Evelina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Indolicidin peptide analogs
                                                                                                                   TYPE: PRT
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                                                                OTHER INFORMATION: Indolicidin peptide analogs
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Pred. No.
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   ; DB 12;
. 3.6e-05;
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3.6e-05;
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               Length 13;
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                                                                                                                            ; OTHER INFORMATION: Indolicidin analog US-10-225-087-4
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US-10-225-087-4
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US-10-225-087-3
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LENGTH: 13
TYPE: PRT
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/225,087
CURRENT FILING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10225087
publication No. US20030171281A1
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: McNicol, Patrica J.
APPLICANT: Fraser, Janet R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: MCNICOL, Patrica J.
APPLICANT: Fraser, Janet R.
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC
TITLE OF INVENTION: FORMULATIONS THEREOF
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Best Local S
                                                                  Matches
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TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND
TITLE OF INVENTION: FORMULATIONS THEREOF
FILE REFERENCE: 660081.417
                                                                                                                                                                                            LENGTH: 13
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2003-01-10
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                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Indolicidin analog
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                                  1 ILPWKWPWWPWRR 13
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13; Conserv
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ILPWKWPWWPWRR 13
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                                                                  3.6e-05;
hes 0;
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RESULT 11 US-10-109-171-42

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GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND FILE REFERENCE: HELX028
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (13)
; OTHER INFORMATION: AMIDATION
US-10-109-171-42
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US-10-109-171-57
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CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/10109171 Publication No. US20030109452A1 GENERAL INFORMATION:
                                                                                                                                                                        Sequence 2, Application US/10252773 Publication No. US20030131383A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
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APPLICANT: EVERETT, NICHOLAS P.
APPLICANT: LI, QUNIGSHUN
APPLICANT: LAWRENCE, CHRISTOPHER
APPLICANT: LAWRENCE, CHRISTOPHER
APPLICANT: DAVIES, MAELOR H.
TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
TITLE OF INVENTION: DEGRADATION
FILE REFERENCE: INTERLINK 3.0-003
CURRENT APPLICATION NUMBER: US/10/252,773
CURRENT FILING DATE: 2002-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Owen, Donald R.
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TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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ORGANISM: ARTIFICIAL SEQUENCE
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Pred. No. 3.6e-05;
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Pred. No. 3.
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RESULT 15
US-09-030-619-40
; Sequence 40, Application US/09030619B
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LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Krieger
                                                 APPLICANT:
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Best Local
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                                                                                      APPLICANT: APPLICANT:
                                                                                                                                                                            Patent No. US20020035061A1
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/219,179
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09909652 Patent No. US20020025537A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/909,652
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YOUVAN, DOUGLAS C.
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
TITLE OF INVENTION: AND SCREENING COMPOUNDS THAT AFFECT CELL VIABILITY
FILE REFERENCE: 22346-7001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kairos Scientific, Inc. APPLICANT: Bylina, Edward J. APPLICANT: Coleman, William J. APPLICANT: Youvan, Douglas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/106,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Ubiquitin indolicidin fusion protein fragment
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Fraser, Janet R.
West, Michael H.P.
McNicol, Patricia J.
WENTION: COMPOSITIONS AND METHODS FOR TREATING
VENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
VENTION: WITH ANTIBIOTICS
                                                                                                   Taylor, Robert
Erfle, Douglas
                                                                                                                                        Krieger, Timothy J.
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Pred. No.
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Pred. No.
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3.6e-05;
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